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SEQUENCE LISTING

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TECH CENTER 1600/2900

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lee, Wen-Hwa  
Shepard, H. Michael  
Gregory, Richard J.  
Wills, Ken N.  
Maneval, Daniel C.  
Lee, Eva  
Goodrich, David  
Wang, Nan-Ping
- (ii) TITLE OF INVENTION: Cell Cycle Controlling Compositions and Methods of Use
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Townsend and Townsend and Crew LLP
  - (B) STREET: Two Embarcadero Center, Eighth Floor
  - (C) CITY: San Francisco
  - (D) STATE: California
  - (E) COUNTRY: USA
  - (F) ZIP: 94111-3834
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/472,760
  - (B) FILING DATE: 07-JUN-1995
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 07/951,947
  - (B) FILING DATE: 28-SEP-1992
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/276,041
  - (B) FILING DATE: 14-JUL-1994
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 07/764,714
  - (B) FILING DATE: 24-SEP-1991
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 07/265,829
  - (B) FILING DATE: 31-OCT-1988
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/225,099
  - (B) FILING DATE: 08-APR-1994
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/079,207
  - (B) FILING DATE: 17-JUN-1993

- (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: US 07/914,039
    - (B) FILING DATE: 14-JUL-1992
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: US 07/550,877
    - (B) FILING DATE: 11-JUL-1990
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: US 08/058,784
    - (B) FILING DATE: 07-MAY-1993
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: US 07/906,008
    - (B) FILING DATE: 26-JUN-1992
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: US 07/553,905
    - (B) FILING DATE: 16-JUL-1990
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: US 08/306,513
    - (B) FILING DATE: 13-SEP-1994
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: US 08/121,108
    - (B) FILING DATE: 13-SEP-1993
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: US 07/956,472
    - (B) FILING DATE: 02-OCT-1992
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: US 08/126,810
    - (B) FILING DATE: 24-SEP-1993
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: US 07/778,510
    - (B) FILING DATE: 17-OCT-1991
  - (viii) ATTORNEY/AGENT INFORMATION:
    - (A) NAME: Bastian, Kevin L.
    - (B) REGISTRATION NUMBER: 34,774
    - (C) REFERENCE/DOCKET NUMBER: 17726A-000410US
  - (ix) TELECOMMUNICATION INFORMATION:
    - (A) TELEPHONE: (415) 576-0200
    - (B) TELEFAX: (415) 576-0300
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 2994 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION: 139..2922  
 (D) OTHER INFORMATION: /product= "RB protein"  
 /note= "retinoblastoma (RB) gene"

## (ix) FEATURE:

(A) NAME/KEY: -  
 (B) LOCATION: 1273..2922  
 (D) OTHER INFORMATION: /note= "truncated RB protein fragment  
 p56-RB"

## (ix) FEATURE:

(A) NAME/KEY: -  
 (B) LOCATION: 2887..2922  
 (D) OTHER INFORMATION: /note= "RB protein C-terminal peptide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTCCGGTTTT TCTCAGGGGA CGTTGAAATT ATTTTGTAA CGGGAGTCGG GAGAGGACGG	60
GGCGTGCCCC GCGTGCGCGC GCGTCGTCCT CCGCGGCGCT CCTCCACAGC TCGCTGGCTC	120
CCGCCGCGGA AAGGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC	171
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala	
1 5 10	
ACC GCC GCC GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCG CCC	219
Thr Ala Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro	
15 20 25	
CCT CCT GAG GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT	267
Pro Pro Glu Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro	
30 35 40	
CTC GTC AGG CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA	315
Leu Val Arg Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala	
45 50 55	
TTA TGT CAG AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG	363
Leu Cys Gln Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp	
60 65 70 75	
TTA ACT TGG GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT	411
Leu Thr Trp Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr	
80 85 90	
ATT CAA AAG AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA	459
Ile Gln Lys Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala	
95 100 105	
GTT GAC CTA GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC	507
Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn	
110 115 120	
ATA GAA ATC AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT	555
Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp	
125 130 135	

ACC	AGT	ACC	AAA	GTT	GAT	AAT	GCT	ATG	TCA	AGA	CTG	TTG	AAG	AAG	TAT	603
Thr	Ser	Thr	Lys	Val	Asp	Asn	Ala	Met	Ser	Arg	Leu	Leu	Lys	Lys	Tyr	
140					145					150					155	
GAT	GTA	TTG	TTT	GCA	CTC	TTC	AGC	AAA	TTG	GAA	AGG	ACA	TGT	GAA	CTT	651
Asp	Val	Leu	Phe	Ala	Leu	Phe	Ser	Lys	Leu	Glu	Arg	Thr	Cys	Glu	Leu	
				160					165					170		
ATA	TAT	TTG	ACA	CAA	CCC	AGC	AGT	TCG	ATA	TCT	ACT	GAA	ATA	AAT	TCT	699
Ile	Tyr	Leu	Thr	Gln	Pro	Ser	Ser	Ser	Ile	Ser	Thr	Glu	Ile	Asn	Ser	
			175					180					185			
GCA	TTG	GTG	CTA	AAA	GTT	TCT	TGG	ATC	ACA	TTT	TTA	TTA	GCT	AAA	GGG	747
Ala	Leu	Val	Leu	Lys	Val	Ser	Trp	Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	
		190					195					200				
GAA	GTA	TTA	CAA	ATG	GAA	GAT	GAT	CTG	GTG	ATT	TCA	TTT	CAG	TTA	ATG	795
Glu	Val	Leu	Gln	Met	Glu	Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	
	205					210					215					
CTA	TGT	GTC	CTT	GAC	TAT	TTT	ATT	AAA	CTC	TCA	CCT	CCC	ATG	TTG	CTC	843
Leu	Cys	Val	Leu	Asp	Tyr	Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	
220					225					230					235	
AAA	GAA	CCA	TAT	AAA	ACA	GCT	GTT	ATA	CCC	ATT	AAT	GGT	TCA	CCT	CGA	891
Lys	Glu	Pro	Tyr	Lys	Thr	Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	
				240					245					250		
ACA	CCC	AGG	CGA	GGT	CAG	AAC	AGG	AGT	GCA	CGG	ATA	GCA	AAA	CAA	CTA	939
Thr	Pro	Arg	Arg	Gly	Gln	Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	
			255					260					265			
GAA	AAT	GAT	ACA	AGA	ATT	ATT	GAA	GTT	CTC	TGT	AAA	GAA	CAT	GAA	TGT	987
Glu	Asn	Asp	Thr	Arg	Ile	Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	
		270					275					280				
AAT	ATA	GAT	GAG	GTG	AAA	AAT	GTT	TAT	TTC	AAA	AAT	TTT	ATA	CCT	TTT	1035
Asn	Ile	Asp	Glu	Val	Lys	Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	
		285				290					295					
ATG	AAT	TCT	CTT	GGA	CTT	GTA	ACA	TCT	AAT	GGA	CTT	CCA	GAG	GTT	GAA	1083
Met	Asn	Ser	Leu	Gly	Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	
300				305						310					315	
AAT	CTT	TCT	AAA	CGA	TAC	GAA	GAA	ATT	TAT	CTT	AAA	AAT	AAA	GAT	CTA	1131
Asn	Leu	Ser	Lys	Arg	Tyr	Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	
				320					325					330		
GAT	GCA	AGA	TTA	TTT	TTG	GAT	CAT	GAT	AAA	ACT	CTT	CAG	ACT	GAT	TCT	1179
Asp	Ala	Arg	Leu	Phe	Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	
			335					340					345			
ATA	GAC	AGT	TTT	GAA	ACA	CAG	AGA	ACA	CCA	CGA	AAA	AGT	AAC	CTT	GAT	1227
Ile	Asp	Ser	Phe	Glu	Thr	Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	
		350					355					360				
GAA	GAG	GTG	AAT	GTA	ATT	CCT	CCA	CAC	ACT	CCA	GTT	AGG	ACT	GTT	ATG	1275
Glu	Glu	Val	Asn	Val	Ile	Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	
		365				370					375					
AAC	ACT	ATC	CAA	CAA	TTA	ATG	ATG	ATT	TTA	AAT	TCA	GCA	AGT	GAT	CAA	1323

Asn 380	Thr	Ile	Gln	Gln	Leu 385	Met	Met	Ile	Leu	Asn 390	Ser	Ala	Ser	Asp	Gln 395	
CCT Pro	TCA Ser	GAA Glu	AAT Asn	CTG Leu	ATT Ile	TCC Ser	TAT Tyr	TTT Phe	AAC Asn	AAC Asn	TGC Cys	ACA Thr	GTG Val	AAT Asn	CCA Pro	1371
AAA Lys	GAA Glu	AGT Ser	ATA Ile	CTG Leu	AAA Lys	AGA Arg	GTG Val	AAG Lys	GAT Asp	ATA Ile	GGA Gly	TAC Tyr	ATC Ile	TTT Phe	AAA Lys	1419
GAG Glu	AAA Lys	TTT Phe	GCT Ala	AAA Lys	GCT Ala	GTG Val	GGA Gly	CAG Gln	GGT Gly	TGT Cys	GTC Val	GAA Glu	ATT Ile	GGA Gly	TCA Ser	1467
CAG Gln	CGA Arg	TAC Tyr	AAA Lys	CTT Leu	GGA Gly	GTT Val	CGC Arg	TTG Leu	TAT Tyr	TAC Tyr	CGA Arg	GTA Val	ATG Met	GAA Glu	TCC Ser	1515
ATG Met	CTT Leu	AAA Lys	TCA Ser	GAA Glu	GAA Glu	GAA Glu	CGA Arg	TTA Leu	TCC Ser	ATT Ile	CAA Gln	AAT Asn	TTT Phe	AGC Ser	AAA Lys	1563
CTT Leu	CTG Leu	AAT Asn	GAC Asp	AAC Asn	ATT Ile	TTT Phe	CAT His	ATG Met	TCT Ser	TTA Leu	TTG Leu	GCG Ala	TGC Cys	GCT Ala	CTT Leu	1611
GAG Glu	GTT Val	GTA Val	ATG Met	GCC Ala	ACA Thr	TAT Tyr	AGC Ser	AGA Arg	AGT Ser	ACA Thr	TCT Ser	CAG Gln	AAT Asn	CTT Leu	GAT Asp	1659
TCT Ser	GGA Gly	ACA Thr	GAT Asp	TTG Leu	TCT Ser	TTC Phe	CCA Pro	TGG Trp	ATT Ile	CTG Leu	AAT Asn	GTG Val	CTT Leu	AAT Asn	TTA Leu	1707
AAA Lys	GCC Ala	TTT Phe	GAT Asp	TTT Phe	TAC Tyr	AAA Lys	GTG Val	ATC Ile	GAA Glu	AGT Ser	TTT Phe	ATC Ile	AAA Lys	GCA Ala	GAA Glu	1755
GGC Gly	AAC Asn	TTG Leu	ACA Thr	AGA Arg	GAA Glu	ATG Met	ATA Ile	AAA Lys	CAT His	TTA Leu	GAA Glu	CGA Arg	TGT Cys	GAA Glu	CAT His	1803
CGA Arg	ATC Ile	ATG Met	GAA Glu	TCC Ser	CTT Leu	GCA Ala	TGG Trp	CTC Leu	TCA Ser	GAT Asp	TCA Ser	CCT Pro	TTA Leu	TTT Phe	GAT Asp	1851
CTT Leu	ATT Ile	AAA Lys	CAA Gln	TCA Ser	AAG Lys	GAC Asp	CGA Arg	GAA Glu	GGA Gly	CCA Pro	ACT Thr	GAT Asp	CAC His	CTT Leu	GAA Glu	1899
TCT Ser	GCT Ala	TGT Cys	CCT Pro	CTT Leu	AAT Asn	CTT Leu	CCT Pro	CTC Leu	CAG Gln	AAT Asn	AAT Asn	CAC His	ACT Thr	GCA Ala	GCA Ala	1947
GAT Asp	ATG Met	TAT Tyr	CTT Leu	TCT Ser	CCT Pro	GTA Val	AGA Arg	TCT Ser	CCA Pro	AAG Lys	AAA Lys	AAA Lys	GGT Gly	TCA Ser	ACT Thr	1995
ACG Thr	CGT Arg	GTA Val	AAT Asn	TCT Ser	ACT Thr	GCA Ala	AAT Asn	GCA Ala	GAG Glu	ACA Thr	CAA Gln	GCA Ala	ACC Thr	TCA Ser	GCC Ala	2043

620		625		630		635	
TTC CAG ACC CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT							2091
Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr							
		640		645		650	
AAA AAA GTG TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA							2139
Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu							
		655		660		665	
CGC CTT CTG TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT							2187
Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu							
		670		675		680	
TTC CAG CAC ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT							2235
Phe Gln His Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His							
		685		690		695	
TTG GAC CAA ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG							2283
Leu Asp Gln Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys							
		700		705		710	
AAT ATA GAC CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT							2331
Asn Ile Asp Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu							
		720		725		730	
CCT CAT GCT GTT CAG GAG ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG							2379
Pro His Ala Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu							
		735		740		745	
GAG TAT GAT TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA							2427
Glu Tyr Asp Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg							
		750		755		760	
CTG AAA ACA AAT ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG							2475
Leu Lys Thr Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu							
		765		770		775	
TCA CCA ATA CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA							2523
Ser Pro Ile Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser							
		780		785		790	
CCC TTA CGG ATT CCT GGA GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT							2571
Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser							
		800		805		810	
CCA TAT AAA ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA							2619
Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro							
		815		820		825	
AGA TCA AGA ATC TTA GTA TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG							2667
Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu							
		830		835		840	
AAG TTC CAG AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC							2715
Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu							
		845		850		855	
AAA AGA AGT GCT GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA							2763
Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu							
		860		865		870	
							875

CGC TTT GAT ATT GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC	2811
Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu	
880 885 890	
CCA GGA GAG TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT	2859
Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr	
895 900 905	
CGA ACA CGA ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA	2907
Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser	
910 915 920	
AAC AAG GAA GAG AAA TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT	2962
Asn Lys Glu Glu Lys	
925	
GGATTCATTG TCTCTCACAG ATGTGACTGT AT	2994

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala Ala Ala	
1 5 10 15	
Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Pro Glu Glu Asp	
20 25 30	
Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg Leu Glu	
35 40 45	
Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln Lys Leu	
50 55 60	
Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu Lys	
65 70 75 80	
Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys Lys	
85 90 95	
Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu Asp Glu	
100 105 110	
Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile Ser Val	
115 120 125	
His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys Val	
130 135 140	
Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala	
145 150 155 160	

Leu	Phe	Ser	Lys	Leu	Glu	Arg	Thr	Cys	Glu	Leu	Ile	Tyr	Leu	Thr	Gln			
				165					170					175				
Pro	Ser	Ser	Ser	Ile	Ser	Thr	Glu	Ile	Asn	Ser	Ala	Leu	Val	Leu	Lys			
			180					185					190					
Val	Ser	Trp	Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	Glu	Val	Leu	Gln	Met			
		195					200					205						
Glu	Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	Leu	Cys	Val	Leu	Asp			
	210					215					220							
Tyr	Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	Lys	Glu	Pro	Tyr	Lys			
225					230					235					240			
Thr	Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	Thr	Pro	Arg	Arg	Gly			
				245					250					255				
Gln	Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	Glu	Asn	Asp	Thr	Arg			
			260					265					270					
Ile	Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	Asn	Ile	Asp	Glu	Val			
		275					280					285						
Lys	Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	Met	Asn	Ser	Leu	Gly			
	290					295					300							
Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	Asn	Leu	Ser	Lys	Arg			
305					310					315					320			
Tyr	Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	Asp	Ala	Arg	Leu	Phe			
				325					330					335				
Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	Ile	Asp	Ser	Phe	Glu			
			340					345					350					
Thr	Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	Glu	Glu	Val	Asn	Val			
		355					360					365						
Ile	Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	Asn	Thr	Ile	Gln	Gln			
	370					375					380							
Leu	Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	Pro	Ser	Glu	Asn	Leu			
385					390					395					400			
Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser	Ile	Leu			
				405					410					415				
Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys	Phe	Ala	Lys			
			420					425					430					
Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	Gln	Arg	Tyr	Lys	Leu			
		435					440					445						
Gly	Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	Met	Leu	Lys	Ser	Glu			
	450					455					460							
Glu	Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	Leu	Leu	Asn	Asp	Asn			
465					470					475				480				
Ile	Phe	His	Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	Glu	Val	Val	Met	Ala			

485					490					495					
Thr	Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	Ser	Gly	Thr	Asp	Leu
			500					505					510		
Ser	Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	Lys	Ala	Phe	Asp	Phe
		515					520					525			
Tyr	Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	Gly	Asn	Leu	Thr	Arg
	530					535					540				
Glu	Met	Ile	Lys	His	Leu	Glu	Arg	Cys	Glu	His	Arg	Ile	Met	Glu	Ser
545					550					555					560
Leu	Ala	Trp	Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	Leu	Ile	Lys	Gln	Ser
				565					570					575	
Lys	Asp	Arg	Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	Ser	Ala	Cys	Pro	Leu
			580					585					590		
Asn	Leu	Pro	Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	Asp	Met	Tyr	Leu	Ser
		595					600					605			
Pro	Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	Thr	Arg	Val	Asn	Ser
	610					615					620				
Thr	Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	Phe	Gln	Thr	Gln	Lys
625					630					635					640
Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	Lys	Lys	Val	Tyr	Arg
				645					650					655	
Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	Arg	Leu	Leu	Ser	Glu
			660					665					670		
His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	Phe	Gln	His	Thr	Leu
		675					680					685			
Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	Leu	Asp	Gln	Ile	Met
	690					695					700				
Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile	Asp	Leu	Lys
705					710					715				720	
Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	Pro	His	Ala	Val	Gln
				725					730					735	
Glu	Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	Glu	Tyr	Asp	Ser	Ile
			740					745					750		
Ile	Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg	Leu	Lys	Thr	Asn	Ile
		755					760					765			
Leu	Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu	Ser	Pro	Ile	Pro	His
	770					775					780				
Ile	Pro	Arg	Ser	Pro	Tyr	Lys	Phe	Pro	Ser	Ser	Pro	Leu	Arg	Ile	Pro
785					790					795				800	
Gly	Gly	Asn	Ile	Tyr	Ile	Ser	Pro	Leu	Lys	Ser	Pro	Tyr	Lys	Ile	Ser
				805					810					815	

Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu  
820 825 830

Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile  
835 840 845

Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu  
850 855 860

Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu  
865 870 875 880

Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys  
885 890 895

Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln  
900 905 910

Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys  
915 920 925